

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hanna, Nabil
Newman, Roland A.
Reff, Mitchell E.
- (ii) TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human Therapy
- (iii) NUMBER OF SEQUENCES: 59
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
(B) STREET: 699 Prince Street
(C) CITY: Alexandria
(D) STATE: VA
(E) COUNTRY: USA
(F) ZIP: 22314-3187
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/523,894
(B) FILING DATE: 06-SEP-1995
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Teskin, Robin L.
(B) REGISTRATION NUMBER: 35,030
(C) REFERENCE/DOCKET NUMBER: 012712-165
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 703-836-6620
(B) TELEFAX: 703-836-2021

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 420 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
(A) ORGANISM: Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: light variable domain of CE9.1

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 4..420

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 61..420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAC	ATG	AAA	CAC	CTG	TGG	TTC	TTC	CTC	CTC	CTG	GTG	GCA	GCC	CCC	AGA	48
Met	Lys	His	Leu	Trp	Phe	Phe	Leu	Leu	Val	Ala	Ala	Pro	Arg			
-19				-15				-10							-5	
TGG	GTC	TTG	TCC	CAG	GTG	CAG	CTG	CAG	GAG	GCG	GGC	CCA	GGA	CTG	GTG	96
Trp	Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Glu	Ala	Gly	Pro	Gly	Leu	Val	
			1			5					10					
AAG	CCT	TCG	GAG	ACC	CTG	TCC	CTC	ACC	TGC	AGT	GTC	TCT	GGT	GGC	TCC	144
Lys	Pro	Ser	Glu	Thr	Leu	Ser	Leu	Thr	Cys	Ser	Val	Ser	Gly	Gly	Ser	
	15				20			25								
ATC	AGC	GGT	GAC	TAT	TAT	TGG	TTC	TGG	ATC	CGC	CAG	TCC	CCA	GGG	AAG	192
Ile	Ser	Gly	Asp	Tyr	Tyr	Trp	Phe	Trp	Ile	Arg	Gln	Ser	Pro	Gly	Lys	
30					35			40								
GGA	CTG	GAG	TGG	ATC	GGC	TAC	ATC	TAT	GGC	AGT	GGT	GGG	GGC	ACC	AAT	240
Gly	Leu	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Gly	Ser	Gly	Gly	Gly	Thr	Asn	
45				50				55							60	
TAC	AAT	CCC	TCC	CTC	AAC	AAT	CGA	GTC	TCC	ATT	TCA	ATA	GAC	ACG	TCC	288
Tyr	Asn	Pro	Ser	Leu	Asn	Asn	Arg	Val	Ser	Ile	Ser	Ile	Asp	Thr	Ser	
			65				70						75			
AAG	AAC	CTC	TTC	TCC	CTG	AAA	CTG	AGG	TCT	GTG	ACC	GCC	GCG	GAC	ACG	336
Lys	Asn	Leu	Phe	Ser	Leu	Lys	Leu	Arg	Ser	Val	Thr	Ala	Ala	Asp	Thr	
			80				85					90				
GCC	GTC	TAT	TAC	TGT	GCG	AGT	AAT	ATA	TTG	AAA	TAT	CTT	CAC	TGG	TTA	384
Ala	Val	Tyr	Tyr	Cys	Ala	Ser	Asn	Ile	Leu	Lys	Tyr	Leu	His	Trp	Leu	
	95					100						105				
TTA	TAC	TGG	GGC	CAG	GGA	GTC	CTG	GTC	ACC	GTC	TCC					420
Leu	Tyr	Trp	Gly	Gln	Gly	Val	Leu	Val	Thr	Val	Ser					
110					115						120					

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp
 -19 -15 -10 -5
 Val Leu Ser Gln Val Gln Leu Gln Glu Ala Gly Pro Gly Leu Val Lys
 1 5 10
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile
 15 20 25
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly
 30 35 40 45
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr
 50 55 60
 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys
 65 70 75
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala
 80 85 90
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu
 95 100 105
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser
 110 115 120

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy variable domain of CE9.1

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 4..387

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 61..387

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACC ATG GCC TGG GCT CTG CTG CTC CTC GGC CTC CTT GCT CAC TTT ACA 48
Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr
-19 -15 -10 -5

GAC TCT GCG GCC TCC TAT GAG TTG AGT CAG CCT CGC TCA GTG TCC GTG 96
Asp Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val
1 5 10

TCC CCA GGA CAG ACG GCC GGG TTC ACC TGT GGG GGA GAC AAC GTT GGA 144
Ser Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly
15 20 25

AGG AAA AGT GTA CAG TGG TAC CAG CAG AAG CCA CCG CAG GCC CCT GTG 192
Arg Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val
30 35 40

CTG GTC ATC TAT GCT GAC AGC GAA CGG CCC TCA GGG ATC CCT GCG CGA 240
Leu Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg
45 50 55 60

TTC TCT GGC TCC AAC TCA GGG AAC ACC GCC ACC CTG ACC ATC AGC GGG 288
Phe Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly
65 70 75

GTC GAG GCC GGG GAT GAG GCT GAC TAT TAC TGT CAG GTG TGG GAC AGT 336
Val Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser
80 85 90

ACT GCT GAT CAT TGG GTC TTC GGC GGA GGG ACC CGG CTG ACC GTC CTA 384
Thr Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu
95 100 105

GGT 387
Gly

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp
-19 -15 -10 -5

Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser
1 5 10

Pro	Gly	Gln	Thr	Ala	Gly	Phe	Thr	Cys	Gly	Gly	Asp	Asn	Val	Gly	Arg
15						20					25				
Lys	Ser	Val	Gln	Trp	Tyr	Gln	Gln	Lys	Pro	Pro	Gln	Ala	Pro	Val	Leu
30					35					40					45
Val	Ile	Tyr	Ala	Asp	Ser	Glu	Arg	Pro	Ser	Gly	Ile	Pro	Ala	Arg	Phe
				50					55					60	
Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	Thr	Leu	Thr	Ile	Ser	Gly	Val
			65					70					75		
Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	Val	Trp	Asp	Ser	Thr
		80					85					90			
Ala	Asp	His	Trp	Val	Phe	Gly	Gly	Gly	Thr	Arg	Leu	Thr	Val	Leu	Gly
95						100					105				

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: lambda variable and constant domains in CE9.1

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 1..702

(ix) FEATURE:

- ```
(A) NAME/KEY: mat_peptide
(B) LOCATION: 1..702
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | GCC | TGG | GCT | CTG | CTG | CTC | CTC | GGC | CTC | CTT | GCT | CAC | TTT | ACA | GAC | 48  |
| Met | Ala | Trp | Ala | Leu | Leu | Leu | Leu | Gly | Leu | Leu | Ala | His | Phe | Thr | Asp |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| TCT | GCG | GCC | TCC | TAT | GAG | TTG | AGT | CAG | CCT | CGC | TCA | GTG | TCC | GTG | TCC | 96  |
| Ser | Ala | Ala | Ser | Tyr | Glu | Leu | Ser | Gln | Pro | Arg | Ser | Val | Ser | Val | Ser |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CCA | GGA | CAG | ACG | GCC | GGG | TTC | ACC | TGT | GGG | GGA | GAC | AAC | GTT | GGA | AGG | 144 |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Gly | Gln | Thr | Ala | Gly | Phe | Thr | Cys | Gly | Gly | Asp | Asn | Val | Gly | Arg |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| AAA | AGT | GTA | CAG | TGG | TAC | CAG | CAG | AAG | CCA | CCG | CAG | GCC | CCT | GTG | CTG | 192 |
| Lys | Ser | Val | Gln | Trp | Tyr | Gln | Gln | Lys | Pro | Pro | Gln | Ala | Pro | Val | Leu |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| GTC | ATC | TAT | GCT | GAC | AGC | GAA | CGG | CCC | TCA | GGG | ATC | CCT | GCG | CGA | TTC | 240 |
| Val | Ile | Tyr | Ala | Asp | Ser | Glu | Arg | Pro | Ser | Gly | Ile | Pro | Ala | Arg | Phe |     |
|     | 65  |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| TCT | GGC | TCC | AAC | TCA | GGG | AAC | ACC | GCC | ACC | CTG | ACC | ATC | AGC | GGG | GTC | 288 |
| Ser | Gly | Ser | Asn | Ser | Gly | Asn | Thr | Ala | Thr | Leu | Thr | Ile | Ser | Gly | Val |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| GAG | GCC | GGG | GAT | GAG | GCT | GAC | TAT | TAC | TGT | CAG | GTG | TGG | GAC | AGT | ACT | 336 |
| Glu | Ala | Gly | Asp | Glu | Ala | Asp | Tyr | Tyr | Cys | Gln | Val | Trp | Asp | Ser | Thr |     |
|     |     |     | 100 |     |     |     | 105 |     |     |     |     |     | 110 |     |     |     |
| GCT | GAT | CAT | TGG | GTC | TTC | GGC | GGA | GGG | ACC | CGG | CTG | ACC | GTC | CTA | GGT | 384 |
| Ala | Asp | His | Trp | Val | Phe | Gly | Gly | Gly | Thr | Arg | Leu | Thr | Val | Leu | Gly |     |
|     |     | 115 |     |     |     | 120 |     |     |     |     |     | 125 |     |     |     |     |
| CAG | CCC | AAG | GCT | GCC | CCC | TCG | GTC | ACT | CTG | TTC | CCG | CCC | TCC | TCT | GAG | 432 |
| Gln | Pro | Lys | Ala | Ala | Pro | Ser | Val | Thr | Leu | Phe | Pro | Pro | Ser | Ser | Glu |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| GAG | CTT | CAA | GCC | AAC | AAG | GCC | ACA | CTG | GTG | TGT | CTC | ATA | AGT | GAC | TTC | 480 |
| Glu | Leu | Gln | Ala | Asn | Lys | Ala | Thr | Leu | Val | Cys | Leu | Ile | Ser | Asp | Phe |     |
|     | 145 |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| TAC | CCG | GGA | GCC | GTG | ACA | GTG | GCC | TGG | AAG | GCA | GAT | AGC | AGC | CCC | GTC | 528 |
| Tyr | Pro | Gly | Ala | Val | Thr | Val | Ala | Trp | Lys | Ala | Asp | Ser | Ser | Pro | Val |     |
|     |     |     |     | 165 |     |     |     | 170 |     |     |     |     |     | 175 |     |     |
| AAG | GCG | GGA | GTG | GAG | ACC | ACC | ACA | CCC | TCC | AAA | CAA | AGC | AAC | AAC | AAG | 576 |
| Lys | Ala | Gly | Val | Glu | Thr | Thr | Thr | Pro | Ser | Lys | Gln | Ser | Asn | Asn | Lys |     |
|     |     |     | 180 |     |     |     |     | 185 |     |     |     |     | 190 |     |     |     |
| TAC | GCG | GCC | AGC | AGC | TAC | CTG | AGC | CTG | ACG | CCT | GAG | CAG | TGG | AAG | TCC | 624 |
| Tyr | Ala | Ala | Ser | Ser | Tyr | Leu | Ser | Leu | Thr | Pro | Glu | Gln | Trp | Lys | Ser |     |
|     |     | 195 |     |     |     | 200 |     |     |     |     |     | 205 |     |     |     |     |
| CAC | AGA | AGC | TAC | AGC | TGC | CAG | GTC | ACG | CAT | GAA | GGG | AGC | ACC | GTG | GAG | 672 |
| His | Arg | Ser | Tyr | Ser | Cys | Gln | Val | Thr | His | Glu | Gly | Ser | Thr | Val | Glu |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| AAG | ACA | GTG | GCC | CCT | ACA | GAA | TGT | TCA | TGA |     |     |     |     |     |     | 702 |
| Lys | Thr | Val | Ala | Pro | Thr | Glu | Cys | Ser | *   |     |     |     |     |     |     |     |
|     | 225 |     |     |     | 230 |     |     |     |     |     |     |     |     |     |     |     |

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ala Trp Ala Leu Leu Leu Leu Gly Leu Leu Ala His Phe Thr Asp  
 1 5 10 15  
 Ser Ala Ala Ser Tyr Glu Leu Ser Gln Pro Arg Ser Val Ser Val Ser  
 20 25 30  
 Pro Gly Gln Thr Ala Gly Phe Thr Cys Gly Gly Asp Asn Val Gly Arg  
 35 40 45  
 Lys Ser Val Gln Trp Tyr Gln Gln Lys Pro Pro Gln Ala Pro Val Leu  
 50 55 60  
 Val Ile Tyr Ala Asp Ser Glu Arg Pro Ser Gly Ile Pro Ala Arg Phe  
 65 70 75 80  
 Ser Gly Ser Asn Ser Gly Asn Thr Ala Thr Leu Thr Ile Ser Gly Val  
 85 90 95  
 Glu Ala Gly Asp Glu Ala Asp Tyr Tyr Cys Gln Val Trp Asp Ser Thr  
 100 105 110  
 Ala Asp His Trp Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly  
 115 120 125  
 Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
 130 135 140  
 Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
 145 150 155 160  
 Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
 165 170 175  
 Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
 180 185 190  
 Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
 195 200 205  
 His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
 210 215 220  
 Lys Thr Val Ala Pro Thr Glu Cys Ser \*  
 225 230

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1404 base pairs

(B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: heavy chain variable and constant gamma  
 4

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..1404

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide  
 (B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AAA | CAC | CTG | TGG | TTC | TTC | CTC | CTC | CTG | GTG | GCA | GCC | CCC | AGA | TGG | 48  |
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
| GTC | TTG | TCC | CAG | GTG | CAG | CTG | CAG | GAG | TCG | GGC | CCA | GGA | CTG | GTG | AAG | 96  |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
| CCT | TCG | GAG | ACC | CTG | TCC | CTC | ACC | TGC | AGT | GTC | TCT | GGT | GGC | TCC | ATC | 144 |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ser | Val | Ser | Gly | Gly | Ser | Ile |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |
| AGC | GGT | GAC | TAT | TAT | TGG | TTC | TGG | ATC | CGC | CAG | TCC | CCA | GGG | AAG | GGA | 192 |
| Ser | Gly | Asp | Tyr | Tyr | Trp | Phe | Trp | Ile | Arg | Gln | Ser | Pro | Gly | Lys | Gly |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | GAG | TGG | ATC | GGC | TAC | ATC | TAT | GGC | AGT | GGT | GGG | GGC | ACC | AAT | TAC | 240 |
| Leu | Glu | Trp | Ile | Gly | Tyr | Ile | Tyr | Gly | Ser | Gly | Gly | Gly | Thr | Asn | Tyr |     |
| 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |     |     |
| AAT | CCC | TCC | CTC | AAC | AAT | CGA | GTC | TCC | ATT | TCA | ATA | GAC | ACG | TCC | AAG | 288 |
| Asn | Pro | Ser | Leu | Asn | Asn | Arg | Val | Ser | Ile | Ser | Ile | Asp | Thr | Ser | Lys |     |
|     |     |     |     | 85  |     |     |     | 90  |     |     |     |     |     | 95  |     |     |
| AAC | CTC | TTC | TCC | CTG | AAA | CTG | AGG | TCT | GTG | ACC | GCC | GCG | GAC | ACG | GCC | 336 |
| Asn | Leu | Phe | Ser | Leu | Lys | Leu | Arg | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTC | TAT | TAC | TGT | GCG | AGT | AAT | ATA | TTG | AAA | TAT | CTT | CAC | TGG | TTA | TTA | 384 |
| Val | Tyr | Tyr | Cys | Ala | Ser | Asn | Ile | Leu | Lys | Tyr | Leu | His | Trp | Leu | Leu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| TAC | TGG | GGC | CAG | GGA | GTC | CTG | GTC | ACC | GTC | TCC | TCA | GCT | AGC | ACC | AAG | 432 |
| Tyr | Trp | Gly | Gln | Gly | Val | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys |     |





|                                                                 |  |     |     |     |      |
|-----------------------------------------------------------------|--|-----|-----|-----|------|
| 355                                                             |  | 360 |     | 365 |      |
| TAC ACC CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC |  |     |     |     | 1152 |
| Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser |  |     |     |     |      |
| 370                                                             |  | 375 |     | 380 |      |
| CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG |  |     |     |     | 1200 |
| Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu |  |     |     |     |      |
| 385                                                             |  | 390 |     | 395 | 400  |
| TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC |  |     |     |     | 1248 |
| Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro |  |     |     |     |      |
| 405                                                             |  |     | 410 |     | 415  |
| GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG |  |     |     |     | 1296 |
| Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val |  |     |     |     |      |
| 420                                                             |  |     | 425 |     | 430  |
| GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG |  |     |     |     | 1344 |
| Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met |  |     |     |     |      |
| 435                                                             |  | 440 |     | 445 |      |
| CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT |  |     |     |     | 1392 |
| His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser |  |     |     |     |      |
| 450                                                             |  | 455 |     | 460 |      |
| CTG GGT AAA TGA                                                 |  |     |     |     | 1404 |
| Leu Gly Lys *                                                   |  |     |     |     |      |
| 465                                                             |  |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ser | Val | Ser | Gly | Gly | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Asp | Tyr | Tyr | Trp | Phe | Trp | Ile | Arg | Gln | Ser | Pro | Gly | Lys | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |
| Leu | Glu | Trp | Ile | Gly | Tyr | Ile | Tyr | Gly | Ser | Gly | Gly | Gly | Thr | Asn | Tyr |
| 65  |     |     |     |     | 70  |     |     |     | 75  |     |     |     |     |     | 80  |

Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
                     85                    90                    95  
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
                     100                    105                    110  
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
                     115                    120                    125  
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
                     130                    135                    140  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
                     145                    150                    155                    160  
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
                     165                    170                    175  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
                     180                    185                    190  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
                     195                    200                    205  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
                     210                    215                    220  
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
                     225                    230                    235                    240  
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly  
                     245                    250                    255  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
                     260                    265                    270  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
                     275                    280                    285  
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
                     290                    295                    300  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
                     305                    310                    315                    320  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
                     325                    330                    335  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
                     340                    345                    350  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
                     355                    360                    365  
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
                     370                    375                    380

000100-4-22-65

Leu Gly Lys \*  
465

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ATG | AAA | CAC | CTG | TGG | TTC | TTC | CTC | CTC | CTG | GTG | GCA | GCC | CCC | AGA | TGG | 48  |
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |     |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| GTC | TTG | TCC | CAG | GTG | CAG | CTG | CAG | GAG | TCG | GGC | CCA | GGA | CTG | GTG | AAG | 96  |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |     |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |     |
|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
| CCT | TCG | GAG | ACC | CTG | TCC | CTC | ACC | TGC | AGT | GTC | TCT | GGT | GGC | TCC | ATC | 144 |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ser | Val | Ser | Gly | Gly | Ser | Ile |     |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |     |

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| AGC | GGT | GAC | TAT | TAT | TGG | TTC | TGG | ATC | CGC | CAG | TCC | CCA | GGG | AAG | GGA | 192 |
| Ser | Gly | Asp | Tyr | Tyr | Trp | Phe | Trp | Ile | Arg | Gln | Ser | Pro | Gly | Lys | Gly |     |
| 50  |     |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |     |
| CTG | GAG | TGG | ATC | GGC | TAC | ATC | TAT | GGC | AGT | GGT | GGG | GGC | ACC | AAT | TAC | 240 |
| Leu | Glu | Trp | Ile | Gly | Tyr | Ile | Tyr | Gly | Ser | Gly | Gly | Gly | Thr | Asn | Tyr |     |
| 65  |     |     |     |     | 70  |     |     |     |     | 75  |     |     |     |     | 80  |     |
| AAT | CCC | TCC | CTC | AAC | AAT | CGA | GTC | TCC | ATT | TCA | ATA | GAC | ACG | TCC | AAG | 288 |
| Asn | Pro | Ser | Leu | Asn | Asn | Arg | Val | Ser | Ile | Ser | Ile | Asp | Thr | Ser | Lys |     |
|     |     |     |     | 85  |     |     |     |     | 90  |     |     |     |     | 95  |     |     |
| AAC | CTC | TTC | TCC | CTG | AAA | CTG | AGG | TCT | GTG | ACC | GCC | GCG | GAC | ACG | GCC | 336 |
| Asn | Leu | Phe | Ser | Leu | Lys | Leu | Arg | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala |     |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |     |
| GTC | TAT | TAC | TGT | GCG | AGT | AAT | ATA | TTG | AAA | TAT | CTT | CAC | TGG | TTA | TTA | 384 |
| Val | Tyr | Tyr | Cys | Ala | Ser | Asn | Ile | Leu | Lys | Tyr | Leu | His | Trp | Leu | Leu |     |
|     |     | 115 |     |     |     |     | 120 |     |     |     |     | 125 |     |     |     |     |
| TAC | TGG | GGC | CAG | GGA | GTC | CTG | GTC | ACC | GTC | TCC | TCA | GCT | AGC | ACC | AAG | 432 |
| Tyr | Trp | Gly | Gln | Gly | Val | Leu | Val | Thr | Val | Ser | Ser | Ala | Ser | Thr | Lys |     |
|     | 130 |     |     |     |     | 135 |     |     |     |     | 140 |     |     |     |     |     |
| GGG | CCA | TCC | GTC | TTC | CCC | CTG | GCG | CCC | TGC | TCC | AGG | AGC | ACC | TCC | GAG | 480 |
| Gly | Pro | Ser | Val | Phe | Pro | Leu | Ala | Pro | Cys | Ser | Arg | Ser | Thr | Ser | Glu |     |
| 145 |     |     |     |     | 150 |     |     |     |     | 155 |     |     |     |     | 160 |     |
| AGC | ACA | GCC | GCC | CTG | GGC | TGC | CTG | GTC | AAG | GAC | TAC | TTC | CCC | GAA | CCG | 528 |
| Ser | Thr | Ala | Ala | Leu | Gly | Cys | Leu | Val | Lys | Asp | Tyr | Phe | Pro | Glu | Pro |     |
|     |     |     |     | 165 |     |     |     |     | 170 |     |     |     |     | 175 |     |     |
| GTG | ACG | GTG | TCG | TGG | AAC | TCA | GGC | GCC | CTG | ACC | AGC | GGC | GTG | CAC | ACC | 576 |
| Val | Thr | Val | Ser | Trp | Asn | Ser | Gly | Ala | Leu | Thr | Ser | Gly | Val | His | Thr |     |
|     |     |     | 180 |     |     |     | 185 |     |     |     |     |     | 190 |     |     |     |
| TTC | CCG | GCT | GTC | CTA | CAG | TCC | TCA | GGA | CTC | TAC | TCC | CTC | AGC | AGC | GTG | 624 |
| Phe | Pro | Ala | Val | Leu | Gln | Ser | Ser | Gly | Leu | Tyr | Ser | Leu | Ser | Ser | Val |     |
|     |     | 195 |     |     |     |     | 200 |     |     |     |     | 205 |     |     |     |     |
| GTG | ACC | GTG | CCC | TCC | AGC | AGC | TTG | GGC | ACG | AAG | ACC | TAC | ACC | TGC | AAC | 672 |
| Val | Thr | Val | Pro | Ser | Ser | Ser | Leu | Gly | Thr | Lys | Thr | Tyr | Thr | Cys | Asn |     |
|     | 210 |     |     |     |     | 215 |     |     |     |     | 220 |     |     |     |     |     |
| GTA | GAT | CAC | AAG | CCC | AGC | AAC | ACC | AAG | GTG | GAC | AAG | AGA | GTT | GAG | TCC | 720 |
| Val | Asp | His | Lys | Pro | Ser | Asn | Thr | Lys | Val | Asp | Lys | Arg | Val | Glu | Ser |     |
| 225 |     |     |     |     | 230 |     |     |     |     | 235 |     |     |     |     | 240 |     |
| AAA | TAT | GGT | CCC | CCA | TGC | CCA | TCA | TGC | CCA | GCA | CCT | GAG | TTC | GAG | GGG | 768 |
| Lys | Tyr | Gly | Pro | Pro | Cys | Pro | Ser | Cys | Pro | Ala | Pro | Glu | Phe | Glu | Gly |     |
|     |     |     |     | 245 |     |     |     |     | 250 |     |     |     |     | 255 |     |     |
| GGA | CCA | TCA | GTC | TTC | CTG | TTC | CCC | CCA | AAA | CCC | AAG | GAC | ACT | CTC | ATG | 816 |
| Gly | Pro | Ser | Val | Phe | Leu | Phe | Pro | Pro | Lys | Pro | Lys | Asp | Thr | Leu | Met |     |
|     |     |     | 260 |     |     |     | 265 |     |     |     |     |     | 270 |     |     |     |

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|                                                                                                                                                       |      |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|------|
| ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG<br>Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln<br>275 280 285     | 864  |
| GAA GAC CCC GAG GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG<br>Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val<br>290 295 300     | 912  |
| CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TTC AAC AGC ACG TAC<br>His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr<br>305 310 315 320 | 960  |
| CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAC GGC<br>Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly<br>325 330 335     | 1008 |
| AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC<br>Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile<br>340 345 350     | 1056 |
| GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG<br>Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val<br>355 360 365     | 1104 |
| TAC ACC CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC<br>Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser<br>370 375 380     | 1152 |
| CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG<br>Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu<br>385 390 395 400 | 1200 |
| TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC<br>Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro<br>405 410 415     | 1248 |
| GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG<br>Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val<br>420 425 430     | 1296 |
| GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG<br>Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met<br>435 440 445     | 1344 |
| CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT<br>His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser<br>450 455 460     | 1392 |
| CTG GGT AAA TGA<br>Leu Gly Lys *                                                                                                                      | 1404 |
| 465                                                                                                                                                   |      |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID.NO:10:

Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp  
 1 5 10 15  
 Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys  
 20 25 30  
 Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile  
 35 40 45  
 Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly  
 50 55 60  
 Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr  
 65 70 75 80  
 Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys  
 85 90 95  
 Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala  
 100 105 110  
 Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu  
 115 120 125  
 Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
 130 135 140  
 Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
 145 150 155 160  
 Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
 165 170 175  
 Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
 180 185 190  
 Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
 195 200 205  
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
 210 215 220  
 Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
 225 230 235 240  
 Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Glu Gly  
 245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 260 265 270  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
 275 280 285  
 Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 290 295 300  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
 305 310 315 320  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 325 330 335  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
 340 345 350  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 355 360 365  
 Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
 370 375 380  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 385 390 395 400  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
 405 410 415  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val  
 420 425 430  
 Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met  
 435 440 445  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 450 455 460  
 Leu Gly Lys \*  
 465

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(viii) POSITION IN GENOME:



(A) CHROMOSOME/SEGMENT: heavy chain gamma 4 with the P and E mutation

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1404

(ix) FEATURE:

(A) NAME/KEY: mat\_peptide

(B) LOCATION: 1..1404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|                                                                 |     |
|-----------------------------------------------------------------|-----|
| ATG AAA CAC CTG TGG TTC TTC CTC CTC CTG GTG GCA GCC CCC AGA TGG | 48  |
| Met Lys His Leu Trp Phe Phe Leu Leu Leu Val Ala Ala Pro Arg Trp |     |
| 1 5 10 15                                                       |     |
| GTC TTG TCC CAG GTG CAG CTG CAG GAG TCG GGC CCA GGA CTG GTG AAG | 96  |
| Val Leu Ser Gln Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys |     |
| 20 25 30                                                        |     |
| CCT TCG GAG ACC CTG TCC CTC ACC TGC AGT GTC TCT GGT GGC TCC ATC | 144 |
| Pro Ser Glu Thr Leu Ser Leu Thr Cys Ser Val Ser Gly Gly Ser Ile |     |
| 35 40 45                                                        |     |
| AGC GGT GAC TAT TAT TGG TTC TGG ATC CGC CAG TCC CCA GGG AAG GGA | 192 |
| Ser Gly Asp Tyr Tyr Trp Phe Trp Ile Arg Gln Ser Pro Gly Lys Gly |     |
| 50 55 60                                                        |     |
| CTG GAG TGG ATC GGC TAC ATC TAT GGC AGT GGT GGG GGC ACC AAT TAC | 240 |
| Leu Glu Trp Ile Gly Tyr Ile Tyr Gly Ser Gly Gly Gly Thr Asn Tyr |     |
| 65 70 75 80                                                     |     |
| AAT CCC TCC CTC AAC AAT CGA GTC TCC ATT TCA ATA GAC ACG TCC AAG | 288 |
| Asn Pro Ser Leu Asn Asn Arg Val Ser Ile Ser Ile Asp Thr Ser Lys |     |
| 85 90 95                                                        |     |
| AAC CTC TTC TCC CTG AAA CTG AGG TCT GTG ACC GCC GCG GAC ACG GCC | 336 |
| Asn Leu Phe Ser Leu Lys Leu Arg Ser Val Thr Ala Ala Asp Thr Ala |     |
| 100 105 110                                                     |     |
| GTC TAT TAC TGT GCG AGT AAT ATA TTG AAA TAT CTT CAC TGG TTA TTA | 384 |
| Val Tyr Tyr Cys Ala Ser Asn Ile Leu Lys Tyr Leu His Trp Leu Leu |     |
| 115 120 125                                                     |     |
| TAC TGG GGC CAG GGA GTC CTG GTC ACC GTC TCC TCA GCT AGC ACC AAG | 432 |
| Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys |     |
| 130 135 140                                                     |     |
| GGG CCA TCC GTC TTC CCC CTG GCG CCC TGC TCC AGG AGC ACC TCC GAG | 480 |
| Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu |     |
| 145 150 155 160                                                 |     |
| AGC ACA GCC GCC CTG GGC TGC CTG GTC AAG GAC TAC TTC CCC GAA CCG | 528 |
| Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro |     |

|                                                                                                                                    |     |     |     |      |     |  |
|------------------------------------------------------------------------------------------------------------------------------------|-----|-----|-----|------|-----|--|
|                                                                                                                                    | 165 |     | 170 |      | 175 |  |
| GTG ACG GTG TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC GTG CAC ACC<br>Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr | 180 | 185 | 190 | 576  |     |  |
| TTC CCG GCT GTC CTA CAG TCC TCA GGA CTC TAC TCC CTC AGC AGC GTG<br>Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val | 195 | 200 | 205 | 624  |     |  |
| GTG ACC GTG CCC TCC AGC AGC TTG GGC ACG AAG ACC TAC ACC TGC AAC<br>Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn | 210 | 215 | 220 | 672  |     |  |
| GTA GAT CAC AAG CCC AGC AAC ACC AAG GTG GAC AAG AGA GTT GAG TCC<br>Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser | 225 | 230 | 235 | 720  |     |  |
| AAA TAT GGT CCC CCA TGC CCA CCA TGC CCA GCA CCT GAG TTC GAG GGG<br>Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly | 245 | 250 | 255 | 768  |     |  |
| GGA CCA TCA GTC TTC CTG TTC CCC CCA AAA CCC AAG GAC ACT CTC ATG<br>Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met | 260 | 265 | 270 | 816  |     |  |
| ATC TCC CGG ACC CCT GAG GTC ACG TGC GTG GTG GTG GAC GTG AGC CAG<br>Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln | 275 | 280 | 285 | 864  |     |  |
| GAA GAC CCC GAG GTC CAG TTC AAC TGG TAC GTG GAT GGC GTG GAG GTG<br>Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val | 290 | 295 | 300 | 912  |     |  |
| CAT AAT GCC AAG ACA AAG CCG CGG GAG GAG CAG TTC AAC AGC ACN TAC<br>His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr | 305 | 310 | 315 | 960  |     |  |
| CGT GTG GTC AGC GTC CTC ACC GTC CTG CAC CAG GAC TGG CTG AAC GGC<br>Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly | 325 | 330 | 335 | 1008 |     |  |
| AAG GAG TAC AAG TGC AAG GTC TCC AAC AAA GGC CTC CCG TCC TCC ATC<br>Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile | 340 | 345 | 350 | 1056 |     |  |
| GAG AAA ACC ATC TCC AAA GCC AAA GGG CAG CCC CGA GAG CCA CAG GTG<br>Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val | 355 | 360 | 365 | 1104 |     |  |
| TAC ACC CTG CCC CCA TCC CAG GAG GAG ATG ACC AAG AAC CAG GTC AGC<br>Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser | 370 | 375 | 380 | 1152 |     |  |
| CTG ACC TGC CTG GTC AAA GGC TTC TAC CCC AGC GAC ATC GCC GTG GAG<br>Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu |     |     |     | 1200 |     |  |

| 385                                                             | 390 | 395 | 400 |      |
|-----------------------------------------------------------------|-----|-----|-----|------|
| TGG GAG AGC AAT GGG CAG CCG GAG AAC AAC TAC AAG ACC ACG CCT CCC |     |     |     | 1248 |
| Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro | 405 | 410 | 415 |      |
| GTG CTG GAC TCC GAC GGC TCC TTC TTC CTC TAC AGC AGG CTA ACC GTG |     |     |     | 1296 |
| Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val | 420 | 425 | 430 |      |
| GAC AAG AGC AGG TGG CAG GAG GGG AAT GTC TTC TCA TGC TCC GTG ATG |     |     |     | 1344 |
| Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met | 435 | 440 | 445 |      |
| CAT GAG GCT CTG CAC AAC CAC TAC ACA CAG AAG AGC CTC TCC CTG TCT |     |     |     | 1392 |
| His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser | 450 | 455 | 460 |      |
| CTG GGT AAA TGA                                                 |     |     |     | 1404 |
| Leu Gly Lys *                                                   |     |     |     |      |
| 465                                                             |     |     |     |      |

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Lys | His | Leu | Trp | Phe | Phe | Leu | Leu | Leu | Val | Ala | Ala | Pro | Arg | Trp |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Val | Leu | Ser | Gln | Val | Gln | Leu | Gln | Glu | Ser | Gly | Pro | Gly | Leu | Val | Lys |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Pro | Ser | Glu | Thr | Leu | Ser | Leu | Thr | Cys | Ser | Val | Ser | Gly | Gly | Ser | Ile |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Ser | Gly | Asp | Tyr | Tyr | Trp | Phe | Trp | Ile | Arg | Gln | Ser | Pro | Gly | Lys | Gly |
|     | 50  |     |     |     |     | 55  |     |     |     | 60  |     |     |     |     |     |
| Leu | Glu | Trp | Ile | Gly | Tyr | Ile | Tyr | Gly | Ser | Gly | Gly | Gly | Thr | Asn | Tyr |
|     | 65  |     |     |     | 70  |     |     |     | 75  |     |     |     |     | 80  |     |
| Asn | Pro | Ser | Leu | Asn | Asn | Arg | Val | Ser | Ile | Ser | Ile | Asp | Thr | Ser | Lys |
|     |     |     | 85  |     |     |     |     | 90  |     |     |     |     |     | 95  |     |
| Asn | Leu | Phe | Ser | Leu | Lys | Leu | Arg | Ser | Val | Thr | Ala | Ala | Asp | Thr | Ala |
|     |     |     | 100 |     |     |     |     | 105 |     |     |     |     | 110 |     |     |
| Val | Tyr | Tyr | Cys | Ala | Ser | Asn | Ile | Leu | Lys | Tyr | Leu | His | Trp | Leu | Leu |

000120-41621960

115 120 125

Tyr Trp Gly Gln Gly Val Leu Val Thr Val Ser Ser Ala Ser Thr Lys  
130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Cys Ser Arg Ser Thr Ser Glu  
145 150 155 160

Ser Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro  
165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr  
180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val  
195 200 205

Val Thr Val Pro Ser Ser Ser Leu Gly Thr Lys Thr Tyr Thr Cys Asn  
210 215 220

Val Asp His Lys Pro Ser Asn Thr Lys Val Asp Lys Arg Val Glu Ser  
225 230 235 240

Lys Tyr Gly Pro Pro Cys Pro Pro Cys Pro Ala Pro Glu Phe Glu Gly  
245 250 255

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
260 265 270

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln  
275 280 285

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
290 295 300

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr  
305 310 315 320

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
325 330 335

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile  
340 345 350

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
355 360 365

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser  
370 375 380

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
385 390 395 400

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro  
405 410 415

(2) INFORMATION FOR SEQ ID NO:13:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

26

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iv) ANTI-SENSE: NO
- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Human or Monkey
- (viii) POSITION IN GENOME:
- (A) CHROMOSOME/SEGMENT: VH2 leader sequence

31

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 29 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ACTAAGTCGA CATGGAGTTT GGGCTGAGC

29

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH4 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ACTAAGTCGA CATGAAACAC CTGTGGTTCT T

31

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 31 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH5 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACTAAGTCGA CATGGGGTCA ACCGCCATCC T

31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH6 leader sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTAAGTCGA CATGTCTGTC TCCTTCCTCA T

31

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

000123456789

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

## (viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH1 leader sequence with MluI site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCAGCAGCY ACGCGTGCCC ACTCCGAGGT

30

## (2) INFORMATION FOR SEQ ID NO:20:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

## (viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH2 leader sequence with MluI site

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GACCGTCCCG ACGCGTGTYT TGTCCCAGGT

30

## (2) INFORMATION FOR SEQ ID NO:21:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

## (vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

## (viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 leader sequence with MluI site



GCTATTTTCA CGCGTGTCCA GTGTGAG

27

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH4 leader sequence with MluI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCGGCTCCCA CGCGTGTCTT GTCCCAG

27

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 30 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH5 leader sequence with MluI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GGCTGTTCTC ACGCGTGTCT GTGCCGAGGT

30

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs



(A) ORGANISM: Human or Monkey

(A) CHROMOSOME/SEGMENT: VH3b primer with XhoI site

GAGGTGCAGC TGCTCGAGTC TGG

23

(D) TOPOLOGY: linear

(iv) ANTI-SENSE: NO

(A) CHROMOSOME/SEGMENT: VH4 primer with XhoI site

CAGGTGCAGC TGCTCGAGTC GGG

23

(D) TOPOLOGY: linear

(A) ORGANISM: Human or Monkey

(A) CHROMOSOME/SEGMENT: VH6 primer with XhoI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGTACAGC TGCTCGAGTC AGG

23

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 26 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgG1-4 primer with NheI site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GGCGGATGCG CTAGCTGAGG AGACGG

26

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATCACAGATC TCTACCATG GTGTTGCAGA CCCAGGTC

38

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

000120-452960

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATCACAGATC TCTCACCATG GRGWCCCCWG CKCAGCT

37

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATCACAGATC TCTCACCATG GACATGAGGG TCCCCGCTCA G

41

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 41 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

000T204T6T950

ATCACAGATC TCTCACCATG GACACVAGGG CCCCCACTCA G

(2) INFORMATION FOR SEQ ID NO:34:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATCACAGATC TCTCACCATG GCCTGGGCTC TGCTGCTCC

39

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

ATCACAGATC TCTCACCATG GCCTGGGCTC CACTACTTC

39

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATCACAGATC TCTCACCATG ACCTGCTCCC CTCTCCTCC

39

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Bgl II site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATCACAGATC TCTCACCATG GCCTGGACTC CTCTCTTTC

39

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 38 base pairs

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

38

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:

- (viii) POSITION IN GENOME:

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

36

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: DNA (genomic)



(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: kappa light chain primer with Kpn1 and BsiW1 sites

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

TGCAGCATCC GTACGTTTGA TTTCCAGCTT

30

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with HindIII and Kpn1 sites

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACCTAGGACG GTAAGCTTGG TACCTCCGCC

30

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

00074047521350

(A) CHROMOSOME/SEGMENT: lambda light chain primer with Kpn 1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACCTAGGACG GTCASSTTGG TACCTCCGCC GAACAC

36

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Human or Monkey

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain primer with AvrII site

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CTTGGGCTGA CCTAGGACGG TCAGCCG

27

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH1 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

CCATGGACTG GACCTGG

17

(2) INFORMATION FOR SEQ ID NO:45:

000720#47527960

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH2 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ATGGACATAC TTTGTTCCAC

20

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: VH3 heavy chain variable region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CCATGGAGTT TGGGCTGAGC

20

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: NO

(viii) POSITION IN GENOME:



- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgM heavy chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TTGGGGCGGA TGCACT

16

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: IgG1-4 heavy chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GATGGGCCCT TGGTGGA

17

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: Kappa light chain variable region

00072044521960

21

21

19

(ii) MOLECULE TYPE: DNA (genomic)

(iv) ANTI-SENSE: YES

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: lambda light chain constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GGAACAGAGT GACCGAGGGG

20

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR primer for human gamma 4 constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGGGGGATCC TCATTACCC AGAGACAGGG

30

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: PCR primer for Human gamma 4 constant region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GGGGGCTAGC ACCAAGGGCC CATCCGTCTT C

31

(2) INFORMATION FOR SEQ ID NO:58:

000720452960

